In the Specification:

On page 1, please amend the "CROSS-REFERENCE TO RELATED APPLICATIONS" paragraph (lines 6-22) as follows:

This application is a continuation of U.S. Application serial number 09/759,130, filed on January 12, 2001.

U.S. Application serial number 09/759,130 ~~This application~~ is a continuation-in-part of U.S. Application serial number 09/479,249, filed on January 7, 2000, and a continuation-in-part of U.S. Application serial number 09/559,497, filed on April 27, 2000.

U.S. Application serial number 09/759,130 ~~This application~~ is also a continuation-in-part of U.S. Application serial number 09/578,063, filed on May 24, 2000, which is a continuation-in-part of U.S. Application serial number 09/333,159, filed on June 14, 1999.

U.S. Application serial number 09/759,130 ~~This application~~ is also a continuation-in-part of U.S. Application serial number 09/596,194, filed on July 14, 2000, which is a continuation-in-part of U.S. Application serial number 09/342,364, filed on June 29, 1999.

U.S. Application serial number 09/759,130 ~~This application~~ is also a continuation-in-part of U.S. Application serial number 09/608,452, filed on June 30, 2000, which is a continuation-in-part of U.S. Application serial number 09/393,996, filed on September 10, 1999.

U.S. Application serial number 09/759,130 ~~This application~~ is also a continuation-in-part of U.S. Application serial number 09/602,871, filed on June 23, 2000, which is a continuation-in-part of U.S. Application serial number 09/420,707, filed on October 19, 1999.

Each of the applications cross-referenced in this section are incorporated into this disclosure by reference in their entirety.

On page 21, please amend the paragraph beginning at line 27 as follows:

Figure 4 comprises Figures 4A through 4H. Figure 4 is an alignment of a portion of the TANGO 416 cDNA sequence ("T416"; residues 1651-4000 of SEQ ID NO: 1) with a human testis cDNA clone having GenBank accession number AL137471 ("AL137471"; SEQ ID NO: 40). This alignment indicates that the two nucleotide sequences are about 98.6% identical over the overlapping region. The alignment was made using the ALIGN software (BLOSUM62 scoring matrix, gap opening penalty 12, gap extension penalty 4, frameshift gap penalty 5). In the alignments in this disclosure, similar residues are indicated by ".", and identical residues are indicated by ":" or "|".

On page 22, please amend the paragraph beginning at line 6 as follows:

Figure 5 comprises Figures 5A through 5O. Figure 5 is an alignment of a portion of the TANGO 416 ORF nucleotide sequence ("T416"; residues 1-3405 of SEQ ID NO: 2) with the ORF nucleotide sequence ("m-PC"; SEQ ID NO: 41) of murine protocadherin (sometimes designated vascular endothelial cadherin-2 or mVE-cad-2). This alignment indicates that the two nucleotide sequences are about 55.4% identical over the overlapping region. The alignment was made using the ALIGN software (BLOSUM62 scoring matrix, gap opening penalty 12, gap extension penalty 4, frameshift gap penalty 5).

On page 22, please amend the paragraph beginning at line 13 as follows:

Figure 6 comprises Figures 6A through 6E. Figure 6 is an alignment of a portion of the TANGO 416 protein amino acid sequence ("T416"; residues 1-1135 of SEQ ID NO: 3) with the amino acid sequence ("m-PC"; SEQ ID NO: 42) of murine protocadherin. This alignment indicates that the two amino acid sequences are about 32.8% identical over the overlapping region. The alignment was made using the ALIGN software (BLOSUM62 scoring matrix, gap opening penalty 12, gap extension penalty 4).

On page 24, please amend the paragraph beginning at line 24 as follows:

Figures 11X-[[6]]1 through 11X-14 is an alignment (made using the Wisconsin™ BestFit software; Smith and Waterman, (1981) Adv. Appl. Math. 2:482-489; gap opening penalty 10 / gap extension penalty 10), of the nucleotide sequences of cDNA molecules encoding form 1a of INTERCEPT 289 ("A"; SEQ ID NO: 81), form 1b of INTERCEPT 289 ("B"; SEQ ID NO: 91), form 2a of INTERCEPT 289 ("C"; SEQ ID NO: 96), form 2b of INTERCEPT 289 ("D"; SEQ ID NO: 101), form 3a of INTERCEPT 289 ("E"; SEQ ID NO: 106), and form 3b of INTERCEPT 289 ("F"; SEQ ID NO: 111).

On pages 32 and 33, please amend the paragraph beginning at line 26 of page 32 as follows:

Figure 26 comprises Figures 26A to 26Q-[[19]]17. The nucleotide sequence (SEQ ID NO: 379) of a cDNA encoding the human TANGO 234 protein described herein is listed in Figures 26A to 26I. The ORF (residues 28 to 4386; SEQ ID NO: 380) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 381) of human TANGO 234 is listed. Figure 26J is a hydrophobicity plot of human TANGO 234 protein. An alignment of the amino acid sequences of human TANGO 234 ("Hum"; SEQ ID NO: 381) and bovine WC1 ("WC1"; SEQ ID NO: 448) proteins is shown in Figures 26K to 26P. An alignment of the nucleotide sequences of an ORF encoding human TANGO 234 ("Hum"; SEQ ID NO: 380) and an ORF encoding bovine WC1 ("WC1"; SEQ ID NO: 449) proteins is shown in Figures 26Q-1 to 26Q-[[19]]17.

On page 34, please amend the paragraph beginning at line 14 as follows:

Figure 30 comprises Figures 30A to 30[[G]]F. The nucleotide sequence (SEQ ID NO: 423) of a cDNA encoding the human INTERCEPT 296 protein described herein is listed in Figures 30A to 30C. The ORF (residues 70 to 1098; SEQ ID NO: 424) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 425) of human INTERCEPT 296 protein is listed. Figure 30D is a hydrophobicity plot of INTERCEPT 296 protein. An alignment of the amino acid sequences of human INTERCEPT 296 protein ("296"; SEQ ID NO: 425) and C. elegans C06E1.3 related protein ("CRP"; SEQ ID NO: 410) is shown in Figures 30E through 30[[G]]F.

On pages 44 and 45, please amend the paragraph beginning at line 20 of page 44 as follows:

Residues 1651-4000 of SEQ ID NO: 1 (the nucleotide sequence of TANGO 416 cDNA) were aligned (using the ALIGN software with gap length penalty of 12, and a gap penalty of 4) with the nucleotide sequence of the human testis cDNA clone DKFZp434B0923 listed in GenBank accession number AL137471. This alignment, shown in Figures 4A-H, was generated using the ALIGN software (using the BLOSUM62 scoring matrix, a gap opening penalty of 12, a gap extension penalty of 4, and a frameshift gap penalty of 5), and indicated 98.6% identity between the two sequences in the 2350-residue overlapping portion. The nucleotide sequence (SEQ ID NO: 2) of the ORF encoding TANGO 416 was aligned using the ALIGN software (with gap length penalty of 12, and a gap penalty of 4)) with the nucleotide sequence of the ORF of a murine protocadherin (GenBank™ accession number Y08715; Telo et al., 1998, J. Biol. Chem. 273:17565-17572), as shown in Figures 5A-O. This alignment was generated using the ALIGN software (using the BLOSUM62 scoring matrix, a gap opening penalty of 12, a gap extension penalty of 4, and a frameshift gap penalty of 5), and indicated 55.4% identity between the two sequences in the overlapping portion. Alignment of the amino acid sequence of TANGO 416 with the amino acid sequence of the murine protocadherin, as shown in Figures 6A-E, indicated 32.8% sequence identity and 42.2 % sequence similarity. This alignment was generated using the ALIGN software (using the BLOSUM62 scoring matrix, a gap opening penalty of 12, a gap extension penalty of 4).

On page 236, please amend the paragraph beginning at line 9 as follows:

TANGO 234 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features, as indicated by the conservation of amino acid sequence between human TANGO 234 protein and bovine WC1 protein, as shown in Figures 26K through 26P, and the conservation of nucleotide sequence between the ORFs encoding human TANGO 234 protein and bovine WC1 protein, as shown in Figures 26Q-1 through 26Q-[[19]]17.

On pages 244 and 245, please amend the paragraph beginning at line 21 of page 244 as follows:

TANGO 234 is likely the human orthologue of ruminant protein WC1, and thus is involved with the physiological processes described above in humans. An alignment of the amino acid sequences of (human) TANGO 234 and bovine WC1 protein is shown in Figures

26K-26P. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap penalties -12/-4), the proteins are 40.4% identical. An alignment of the nucleotide sequences of the ORFs encoding (human) TANGO 234 and bovine WC1 protein is shown in Figures 26Q-1 to 26Q-[[19]]17. The two ORFs are 54.3% identical, as assessed using the same software and parameters.

On page 269, please amend the paragraph beginning at line 19 as follows:

Figures 30E through 30[[G]]F depicts an alignment of the amino acid sequences of human INTERCEPT 296 protein (SEQ ID NO: 425) and Caenorhabditis elegans C06E1.3 related protein (SEQ ID NO: 410). In this alignment (pam120.mat scoring matrix, gap penalties -12/-4), the amino acid sequences of the proteins are 26.8% identical. The C. elegans protein has five predicted transmembrane domains.